

GenCore version 5.1.4.p5_4578
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OM protein - protein search, using sw model

Run on: May 19, 2003, 16:36:02 ; Search time 15.2044 Seconds
(without alignments)
982.052 Million cell updates/sec

Title: US-09-625-573-4

Perfect score: 1900

Sequence: I MLSTSRFRFINNTNESGEEV.....DGVISTNTPTSGEQEVSNAGL 360

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues 112892

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1845	97.1	360	1	CKR2_HUMAN
2	1651.5	86.9	374	1	CKR2_HUMAN
3	1542	81.2	373	1	CKR2_RAT
4	1535	80.8	373	1	CKR2_MOUSE
5	1396	73.5	354	1	CKP5_MOUSE
6	1386	72.9	354	1	CKR5_RAT
7	1376	72.4	352	1	CKR5_CERTO
8	1371	72.2	352	1	CKR5_HYLLE
9	1370	72.1	352	1	CKR5_MACMU
10	1370	72.1	352	1	CKR5_PANTR
11	1370	72.1	352	1	CKR5_PONPY
12	1368	72.0	352	1	CKR5_GORGO
13	1368	72.0	352	1	CKR5_PAPHA
14	1364	71.8	352	1	CKR5_HUMAN
15	1363	71.7	352	1	CKR5_TRAPH
16	1361	71.6	352	1	CKR5_PYGBI
17	1360	71.6	352	1	CKR5_TRAFR
18	1359	71.5	352	1	CKR5_PYGNE
19	1344	70.7	352	1	CKR5_CERAE
20	1036	54.5	355	1	CKR1_HUMAN
21	1018.5	53.6	359	1	CKR3_MOUSE
22	1003.5	52.8	359	1	CKR3_RAT
23	995	52.4	358	1	CKR3_CAVPO
24	981	51.6	355	1	CKR1_MACMU
25	960.5	50.6	355	1	CKR1_MOUSE
26	947	49.8	355	1	CKR3_HUMAN
27	940.5	49.5	355	1	CKR3_MACMU
28	924.5	48.7	355	1	CKR3_CERAE
29	871	45.8	360	1	CKR4_MOUSE
30	862.5	45.4	360	1	CKR4_HUMAN
31	778.5	41.0	356	1	CKRV_MOUSE
32	751	39.5	355	1	CKR8_HUMAN
33	743.5	39.1	356	1	CKR8_MACMU

34	731.5	38.5	353	1	CKR8_MOUSE	p54484 mus musculus
35	722.5	38.0	354	1	C3X1_RAT	p35411 rattus norvegicus
36	715.5	37.7	354	1	C3X1_MOUSE	Q920d9 mus musculus
37	708	37.3	355	1	C3X1_HUMAN	P49238 homo sapiens
38	599	31.5	384	1	CKD6_HUMAN	O00590 homo sapiens
39	595	31.3	378	1	CKD6_MOUSE	O08707 mus musculus
40	591	31.1	382	1	CKD6_RAT	O09027 rattus norvegicus
41	581.5	30.6	378	1	CKR7_HUMAN	P32248 homo sapiens
42	575	30.3	357	1	CKR9_HUMAN	P51686 homo sapiens
43	571.5	30.1	367	1	CKR6_MOUSE	O54889 mus musculus
44	569	29.9	369	1	CKR9_MOUSE	Q9wtu7 mus musculus
45	569	29.9	378	1	CKR7_MOUSE	P47774 mus musculus

ALIGNMENTS

RESULT 1

ID	CKR2_MACMU	STANDARD;	PRT;	360 AA.
AC	018793:			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	C-C chemokine receptor type 2 (C-CR2) (CCR-2) (CCR2)			
DE	(Monocyte chemoattractant protein 1 receptor) (MCP-1-R) (CCR2).			
GN	CCR2 OR CMKR2.			
OS	Macaca mulatta (Rhesus macaque).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;			
OC	Cercopithecoidea; Macaca.			
OX	NCBI_TaxID=9544;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=21354176; PubMed=11461684;			
RA	Margulies B.J., Hauer D.A., Clements J.E.;			
RT	"Identification and comparison of eleven rhesus macaque chemokine receptors."			
RL	AIDS Res. Hum. Retroviruses 17:981-986(2001).			
CC	-1- FUNCTION: RECEPTOR FOR THE MCP-1, MCP-3 AND MCP-4 CHEMOKINES.			
CC	TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.			
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.			
CC	-1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A AND B (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.			
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.			
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CC	EMBL; AF013958; AAD11572.1; -			
DR	InterPro; IPR000276; GPCR_Rhodopsn.			
DR	Pfam; PF00001; 7tm_1; 1.			
DR	PRINTS; PR00237; GPCRHOOPS.			
DR	PROSITE; PS00237; G_PROTEIN_RECEPTOR_1; 1.			
DR	PROSITE; PS00262; G_PROTEIN_RECEPTOR_2; 1.			
KW	G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation; Alternative splicing.			
KW	DOMAIN 1 42			
FT	TRANSMEM 43 70			
FT	TRANSMEM 71 80			
FT	TRANSMEM 81 100			
FT	TRANSMEM 101 114			
FT	TRANSMEM 115 136			
FT	TRANSMEM 137 153			
FT	TRANSMEM 154 178			
FT	TRANSMEM 179 206			
FT	TRANSMEM 207 226			

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FT DOMAIN 227 243 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 244 268 6 (POTENTIAL).
FT DOMAIN 269 285 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 286 309 7 (POTENTIAL).
FT DOMAIN 310 360 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 14 14 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT MOD_RES 26 26 SULFATION (BY SIMILARITY).
FT DISULFID 113 190 BY SIMILARITY.
SQ SEQUENCE 360 AA; 41139 MW; 4B2552BCE913FE9F CRC64;

Query Match
Best Local Similarity 96.9%; Pred. No. 1.3e-101; Length 360;
Matches 349; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 MLSTSRFRIRNTNNGSEEVTFEDYDYGAPCHKFDVKQIGQALLPPLYSLVFIQFVGN 60
DB 1 MLSTSRFRIRNTNNGSEEVTFEDYDYGAPCHKFDVKQIGQALLPPLYSLVFIQFVGN 60
QY 61 MLVLLILNCKKLKCLTDIYLLNLAISSDLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
DB 61 MLVLLILNCKKLKCLTDIYLLNLAISSDLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
QY 121 HIGYFGGIFIIILLTDRLYLAIHVAFFALKARTVTFGVVTSVITLWVAFASVPGIIFTK 180
DB 121 HIGYFGGIFIIILLTDRLYLAIHVAFFALKARTVTFGVVTSVITLWVAFASVPGIIFTK 180
QY 181 COKEDSVYVCGPFRGNWPHIMRNILGLVPLIMVICYSGILKTLRCRNEKKRHR 240
DB 181 COKEDSVYVCGPFRGNWPHIMRNILGLVPLIMVICYSGILKTLRCRNEKKRHR 240
QY 241 AVRVTFTIMVFLFWTPNIVILLTFQFFGLSNCESTSQLDOATQVTTGLMTHCCI 300
DB 241 AVRVTFTIMVFLFWTPNIVILLTFQFFGLSNCESTSQLDOATQVTTGLMTHCCI 300
QY 301 NPITIAVGEKFRRLSVFPRKHITRCKQCPVFYRETVGVTSNTPSTGQEVSAAGL 360
DB 301 NPITIAVGEKFRRLSVFPRKHITRCKQCPVFYRETVGVTSNTPSTGQEVSAAGL 360

RESULT 2
CKR2_HUMAN
ID CKR2_HUMAN STANDARD; PRT; 374 AA.
AC P41597;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 2 (C-C CKR-2) (CCR-2) (CCR2)
DE (Monocyte chemoattractant protein 1 receptor) (MCP-1-R) (CCR2).
DE CCR2 OR CMKBR2.
OC Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94195821; PubMed=8146186;
RA Charo I.F., Myers S.J., Herman A., Franci C., Connolly A.J.,
RA Coughlin S.R.;
RT "Molecular cloning and functional expression of two monocyte
RT chemoattractant protein 1 receptors reveals alternative splicing of
RT the carboxyl-terminal tails.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:2752-2756(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94324942; PubMed=8048929;
RA Yamagami S., Tokuda Y., Ishii K., Tamaka H., Endo N.;
RT "cDNA cloning and functional expression of a human monocyte
RT chemoattractant protein 1 receptor.";
RL Biochem. Biophys. Res. Commun. 202:1156-1162(1994).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=97150864; PubMed=8995400;
RA Wong L.-M., Myers S.J., Tsou C.-L., Gosling J., Arai H., Charo I.F.;

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RT "Organization and differential expression of the human monocyte
RT chemoattractant protein 1 receptor gene. Evidence for the role of the
RL carboxyl-terminal tail in receptor trafficking.";
RN J. Biol. Chem. 272:1038-1045(1997).
RP [4]
RA McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,
RA Nham M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz K.,
RA Gnoj L., la Bastide M., Kaplan N., Greco T., Touchman J.,
RA Muzny D., Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M.,
RA Porcel B.M., Dragan Y., Giacalone J., Pae A., Powell E.,
RA Solinsky K.A., Desilva U., Diaz-Perez S., Zhou X., Yu Y.,
RA Watanabe M., Doggett N., Garcia D., Sagripanti J.L.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SULFATION OF TYR-26, AND N-GLYCOSYLATION.
RX MEDLINE=20501139; PubMed=11046064;
RA Preobrazhensky A.A., Dragan S., Kawano T., Gavrilin M.A., Gulina I.V.,
RA Chakravarty L., Kolattukudy P.E.;
RT "Monocyte chemotactic protein-1 receptor CCR2B is a glycoprotein that
RT has tyrosine sulfation in a conserved extracellular N-terminal
RL region.";
RN J. Immunol. 165:5295-5303(2000).
RP -1- FUNCTION: Receptor for the MCP-1, MCP-3 and MCP-4 chemokines.
CC Transduces a signal by increasing the intracellular calcium ions
CC level. Alternative coreceptor with CD4 for HIV-1 infection.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A (SHOWN HERE) AND B; ARE
CC PRODUCED BY ALTERNATIVE SPLICING.
CC -1- PTM: N-GLYCOSYLATED.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC
CC EMBL; U03882; AAA19119.1; -
CC EMBL; U03905; AAA19120.1; -
CC EMBL; D29884; BAA06253.1; -
CC EMBL; U80924; AAC51637.1; -
CC EMBL; U80924; AAC51637.1; -
CC EMBL; U95626; AAB57791.1; -
CC EMBL; U95626; AAB57792.1; -
CC Genew; HGNC:1603; CCR2.
CC MIM; 601267; -
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm_1; 1.
CC PRINTS; PR00237; GPCRHHODPSN.
CC PROSITE; PS00237; G_PROTEIN_RECF1_1; 1.
CC PROSITE; PS00262; G_PROTEIN_RECF1_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation;
KW Alternative splicing.
FT DOMAIN 1 42 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 43 70 1 (POTENTIAL).
FT DOMAIN 71 80 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 81 100 2 (POTENTIAL).
FT DOMAIN 101 114 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 115 136 3 (POTENTIAL).
FT DOMAIN 137 153 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 154 178 4 (POTENTIAL).
FT DOMAIN 179 206 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 207 226 5 (POTENTIAL).
FT DOMAIN 227 243 6 (POTENTIAL).
FT TRANSMEM 244 268 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 269 285 7 (POTENTIAL).
FT TRANSMEM 310 374 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 14 14 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT MOD_RES 26 26 SULFATION.

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FT DISULFID 113 190 BY SIMILARITY.
 FT VARSPLIC 314 374 SLFHIALGRIAPLQKPGVGRGNKVVTTQGLDGR
 FT GKGSIGRAISLQDEKA -> RYLSVFFRKHIKRECK
 FT QCPVYFRETVDGVTSTNTSTGEQVSAGL (IN
 FT ISOFORM B).
 SQ SEQUENCE 374 AA; 41914 MW; F865E0D39E74CF0F CRC64;

Query Match 86.9%; Score 1651.5; DB 1; Length 374;
 Best Local Similarity 95.5%; Pred. No. 2.7e-90;
 Matches 319; Conservative 3; Mismatches 5; Indels 7; Gaps 3;

QY 1 MLSTSRFRIRNTNESGEVTTFFDYDYGAPCHKFDVKQIGAOQLPPLYSLVFTFGVGN 60
 DB 1 MLSTSRFRIRNTNESGEVTTFFDYDYGAPCHKFDVKQIGAOQLPPLYSLVFTFGVGN 60
 QY 61 MLVVLILINCKKLCUFDIYLLNLAISDLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
 DB 61 MLVVLILINCKKLCUFDIYLLNLAISDLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
 QY 121 HIGYFGGIFPILLTIDRYLAIVHAFKARTVTFGVTSVITLWVAFASVPGIIFTK 180
 DB 121 HIGYFGGIFPILLTIDRYLAIVHAFKARTVTFGVTSVITLWVAFASVPGIIFTK 180
 QY 181 CQKEDSVYVCGPYPRGNNFHTMRNLGLVPLLLMWICYSGLKTLRCRNEKKRHR 240
 DB 181 CQKEDSVYVCGPYPRGNNFHTMRNLGLVPLLLMWICYSGLKTLRCRNEKKRHR 240
 QY 241 AVRVIPTIMIVYFELFWTPYINIVILLNTFQEFGLSNCESTSQLDOAQVTTGLMTHCCI 300
 DB 241 AVRVIPTIMIVYFELFWTPYINIVILLNTFQEFGLSNCESTSQLDOAQVTTGLMTHCCI 300
 QY 301 NPIIYAFVGEKFRYLSVFFRKHIKTRFCQCPV 334
 DB 301 NPIIYAFVGEKFRYLSVFFRKHIKTRFCQCPV 334

RESULT 3
 ID CKR2_RAT STANDARD; PRT; 373 AA.
 AC O5193;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE C-C chemokine receptor type 2 (C-C CKR-2) (CC-CKR-2) (CCR-2) (CCR2).
 GN Rattus norvegicus (Rat).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley;
 RX MEDLINE=98318173; PubMed=9655467;
 RA Jiang Y., Salafraanca M.N., Adhikari S., Xia Y., Peng L., Sonntag M.K.,
 RA deFebre C.M., Pennell N.A., Streit W.J., Harrison J.K.;
 RA "Chemokine receptor expression in cultured glia and rat experimental
 RT allergic encephalomyelitis.";
 RL J. Neuroimmunol. 86:1-12(1998).
 CC -!- FUNCTION: RECEPTOR FOR THE MCP-1 (JE), MCP-3 (FIC) AND MCP-5
 CC CHEMOKINES. TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR
 CC CALCIUM IONS LEVEL (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN LUNG, SPLEEN, KIDNEY, THYMUS AND
 CC MACROPHAGES.
 CC -!- INDUCTION: IN ANIMALS IN WHICH EXPERIMENTAL ALLERGIC
 CC ENCEPHALOMYELITIS (EAE) HAS BEEN INDUCED.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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DR EMBL; U77349; AAC03242.1; -;
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHHODOPS.
 DR PROSITE; PS00237; G_PROTEIN_RECPT_FL1; 1.
 DR PROSITE; PS00262; G_PROTEIN_RECPT_FL2; 1.
 KW G-protein coupled receptor; transmembrane.
 FT DOMAIN 1 60 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 61 81 POTENTIAL.
 FT DOMAIN 82 91 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 92 112 POTENTIAL.
 FT DOMAIN 113 128 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 129 149 POTENTIAL.
 FT DOMAIN 150 170 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 171 191 POTENTIAL.
 FT DOMAIN 192 220 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 221 241 POTENTIAL.
 FT DOMAIN 242 256 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 257 277 POTENTIAL.
 FT DOMAIN 278 301 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 302 322 POTENTIAL.
 FT DOMAIN 323 373 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 126 203 BY SIMILARITY.
 SQ SEQUENCE 373 AA; 42763 MW; 2E7BB012F5D6D09 CRC64;

Query Match 81.2%; Score 1542; DB 1; Length 373;
 Best Local Similarity 80.0%; Pred. No. 6.8e-84;
 Matches 288; Conservative 24; Mismatches 48; Indels 0; Gaps 0;

QY 1 MLSTSRFRIRNTNESGEVTTFFDYDYGAPCHKFDVKQIGAOQLPPLYSLVFTFGVGN 60
 DB 14 ILSTSHSLFPRSIQELDEGATTPYDDGEPCHKTSVKQIGAWILPPLYSLVFTFGVGN 73
 QY 61 MLVVLILINCKKLCUFDIYLLNLAISDLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
 DB 74 MLVVLILINCKKLCUFDIYLLNLAISDLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 133
 QY 121 HIGYFGGIFPILLTIDRYLAIVHAFKARTVTFGVTSVITLWVAFASVPGIIFTK 180
 DB 134 HIGYFGGIFPILLTIDRYLAIVHAFKARTVTFGVTSVITLWVAFASVPGIIFTK 193
 QY 181 CQKEDSVYVCGPYPRGNNFHTMRNLGLVPLLLMWICYSGLKTLRCRNEKKRHR 240
 DB 194 SEQEDDQHTCGPYPTIWNKFNQTIMRNILSLILPLLVWVICYSGILTLFCRNEKKRHR 253
 QY 241 AVRVIPTIMIVYFELFWTPYINIVILLNTFQEFGLSNCESTSQLDOAQVTTGLMTHCCI 300
 DB 254 AVRLEIFAIMIVYFELFWTPYINIVILLNTFQEFGLSNCESTSQLDOAQVTTGLMTHCCI 313
 QY 301 NPIIYAFVGEKFRYLSVFFRKHIKTRFCQCPVYRETVDGVTSTNTSTGEQVSAGL 360
 DB 314 NPIIYAFVGEKFRYLSVFFRKHIKTRFCQCPVYRETVDGVTSTNTSTGEQVSAGL 373

RESULT 4
 ID CKR2_MOUSE STANDARD; PRT; 373 AA.
 AC P51683; O61172;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE C-C chemokine receptor type 2 (C-C CKR-2) (CC-CKR-2) (CCR-2) (CCR2)
 DE (JE/FIC receptor) (MCP-1 receptor).
 GN CCR2 OR CMKBR2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.

RX MEDLINE=96205938; PubMed=8631787;
RA Boring L., Gosling J., Montecarlo F.S., Lusis A.J., Tsou C.-L.,
Chao I.F.;
RT "Molecular cloning and functional expression of murine JE (monocyte
chemoattractant protein 1) and murine macrophage inflammatory protein
1 alpha receptors: evidence for two closely linked C-C chemokine
receptors on chromosome 9.";
RL J. Biol. Chem. 271:7551-7558(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX MEDLINE=96216064; PubMed=8662823;
RA Kurihara T., Bravo R.;
RT "Cloning and functional expression of mCCR2, a murine receptor for
the C-C chemokines JE and FIC.";
RL J. Biol. Chem. 271:11603-11606(1996).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=97026720; PubMed=8872898;
RA Heesen M., Tanabe S., Berman M.A., Yoshizawa I., Luo Y., Kim R.,
Post T.W., Gerard C., Dorf M.E.;
RT "Mouse astrocytes respond to the chemokines MCP-1 and KC, but reverse
transcriptase-polymerase chain reaction does not detect mRNA for the
KC or new MCP-1 receptor.";
RL J. Neurosci. Res. 45:382-391(1996).
CC -1- FUNCTION: RECEPTOR FOR THE MCP-1 (JE), MCP-3 (FIC) AND MCP-5
CHEMOKINES. TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR
CALCIUM IONS LEVEL.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: DETECTED IN MONOCYTE/MACROPHAGE CELL LINES,
BUT NOT IN NONHEMATOPOIETIC CELL LINES.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC -----
DR EMBL; U47035; AAC52453.1; -;
DR EMBL; U51717; AAC52557.1; -;
DR EMBL; U56819; AAC52784.1; -;
DR MGD; MGI:106185; Cmkbr2.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1.1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECP_F1.2; 1.
KW G-protein coupled receptor; Transmembrane.
FT DOMAIN 1 55 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 56 83 1 (POTENTIAL).
FT DOMAIN 84 93 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 94 114 2 (POTENTIAL).
FT DOMAIN 115 127 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 128 149 3 (POTENTIAL).
FT DOMAIN 150 166 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 167 191 4 (POTENTIAL).
FT DOMAIN 192 219 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 220 239 5 (POTENTIAL).
FT DOMAIN 240 256 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 257 281 6 (POTENTIAL).
FT DOMAIN 282 298 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 299 322 7 (POTENTIAL).
FT DOMAIN 323 373 CYTOPLASMIC (POTENTIAL).
FT DISULFID 126 203 BY SIMILARITY.
FT CONFLICT 39 Y -> H (IN REF. 1).
FT CONFLICT 184 A -> G (IN REF. 1).
FT CONFLICT 264 V -> G (IN REF. 1).
SQ SEQUENCE 373 AA; 42782 MW; FA012C10F4C9325A CRC64;

Query Match

80.8%; Score 1535; DB 1; Length 373;

Best Local Similarity 79.7%; Pred. No. 1.7e-83;
Matches 287; Conservative 25; Mismatches 48; Indels 0; Gaps 0;

QY 1 MLSTSRFRIRNTNTEGSEEVTFDYDYGAPCHFDVKQIGAOQLPPLYSLVFIQFVGN 60
Db | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
14 ILTSHSLFTRSIQELDEGATPYDYGDEPCHKTSVKQIGAWILPPLYSLVFIQFVGN 73
QY 61 MLVVLILINCKKLCITDIYLLNLAIISDLLELITLPLMAHSAANWVFGNACKLFTGLY 120
Db | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
74 MLVILILGCKKLSMTDIIYLLNLAIISDLLELITLPLMAHSAANWVFGNACKLFTGLY 133
QY 121 HIGYFGGIFPIILLTIDRYLAIVHAFALKARTVTGVTSTVITWLVAFAVSPGLIIFTK 180
Db | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
134 HIGYFGGIFPIILLTIDRYLAIVHAFALKARTVTGVTSTVITWLVAFAVSPGLIIFTK 193
QY 181 CQKEDSVVCGPFGNNPHTIMRNITGLVLPILLIMVICYSGTLKTLRCRNEKKRHR 240
Db | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
194 SKQDDHYTCGPFTQLWKNFQITMRNILLSLILPLLVWVICYSGTLKTLRCRNEKKRHR 253
QY 241 AVRVIPTIMIVYFLWTPYINIVILLNTFQEFGLSNCESTSQLDQATQVTEFLGTHCCI 300
Db | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
254 AVRLPAMIVYFLWTPYINIVILLNTFQEFGLSNCESTSQLDQATQVTEFLGTHCCI 313
QY 301 NPVIYAFVGKFRYLSVFFRKHKHITKRECKQCPFYRTVDGVTSTNTPTSGEQSVSAGL 360
Db | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
314 NPVIYAFVGKFRYLSVFFRKHKHITKRECKQCPFYRTVDGVTSTNTPTSGEQSVSAGL 373

RESULT 5
CKR5_MOUSE
ID CKR5_MOUSE STANDARD; PRT; 354 AA.
AC P51682; O61867; P97405; O35313; P97308; O35891;
DT 01-OCT-1996 (Rel. 34, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (MIP-1
alpha receptor).
GN CCR5 OR CMKR5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutharia; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVJ; TISSUE=Spleen;
RX MEDLINE=96205938; PubMed=8631787;
RA Boring L., Gosling J., Montecarlo F.S., Lusis A.J., Tsou C.-L.,
Chao I.F.;
RT "Molecular cloning and functional expression of murine JE (monocyte
chemoattractant protein 1) and murine macrophage inflammatory protein
1 alpha receptors: evidence for two closely linked C-C chemokine
receptors on chromosome 9.";
RL J. Biol. Chem. 271:7551-7558(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6 X CBA; TISSUE=Thymus;
RX MEDLINE=96278910; PubMed=8662890;
RA Meyer A., Coyle A.J., Proudfoot A.E.I., Wells T.N.C., Power C.A.;
RT "Cloning and characterization of a novel murine macrophage
inflammatory protein-1 alpha receptor.";
RL J. Biol. Chem. 271:14445-14451(1996).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=129/Ola;
RA Kuziel W.A., Beck M.A., Dawson T.C., Maeda N.;
RN Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
RP [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6, and NIH Swiss; TISSUE=Liver, Kidney, and Spleen;
RX MEDLINE=98001387; PubMed=9343222;
RA Kuhnmann S.E., Platt E.J., Kozak S.L., Kabat D.;
RT "Polymorphisms in the CCR5 genes of African green monkeys and mice
implicate specific amino acids in infections by simian and human

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 DR EMBL; Y12009; CAA72737.1; -
 DR EMBL; U77350; AAC03243.1; -
 DR Pfam; IPR000276; GPCR_Rhodpsn.
 DR PRINTS; PR00237; GPCRHHODOPSN.
 DR PROSITE; PS00237; G-PROTEIN RECF_F1_1; 1.
 DR PROSITE; PS00237; G-PROTEIN RECF_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 32 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 33 60 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 61 70 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 71 91 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 92 104 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 105 126 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 127 143 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 144 168 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 169 200 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 201 220 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 221 237 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 238 262 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 263 279 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 280 303 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 304 354 BY SIMILARITY.
 FT DISULFID 103 180 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 270 270
 SQ SEQUENCE 354 AA; 41030 MW; 77EDB368AA4C868D CRC64;

Query Match 72.9%; Score 1386; DB 1; Length 354;

Best Local Similarity 74.9%; Pred. No. 8.6e-75;
 Matches 262; Conservative 30; Mismatches 52; Indels 6; Gaps 2;

Qy 17 GEEVTFEDYD--GAPCHKFDVKQIGAGLLPLPLSLVFIQFVGNMVLILINCKKLK 74
 Db 5 GSIPYIYDIDYMSAPCKVNVKQIAAQLPLSLVFIQFVGNMVLILINCKKLK 64
 Qy 75 CLTDIYLNLAISDLFLITLPLWHAASANEWVFGNAMCKLFTGLYHIGYFGGIFILL 134
 Db 65 SMTDIYLNLAISDLFLITLPLWHAASANEWVFGNAMCKLFTGLYHIGYFGGIFILL 124
 135 TIDRLAIVHAFKARTVTFGVTSVITLWVAFASVPGIIFTKCKEDSVVCGPYF 194
 Db 125 TIDRLAIVHAFKARTVTFGVTSVITLWVAFASVPGIIFTKCKEDSVVCGPYF 184
 Qy 195 ----PRGNWNTIMRNILGLVPLIMVICYSGILKTLILRCNEKRRHRAVFIIMI 250
 Db 185 LHIOYRFKWHFOTLKWVILSLILPLVWVICYSGILTLILRCNEKRRHRAVFIIMI 244
 Qy 251 VYFLEWTPYNIIVLLNTFOEFGSLNCESTSQLDQATQVETGLMTHCCINPIIYAFVGE 310
 Db 245 VYFLEWTPYNIIVLLNTFOEFGSLNCESTSQLDQATQVETGLMTHCCINPIIYAFVGE 304
 Qy 311 KPRNVLVFFRKHITKRFCKQCPVFRETVGVTSNTSTSTGQEVSAAGL 360
 Db 305 KPRNVLVFFRKHITKRFCKQCPVFRETVGVTSNTSTSTGQEVSAAGL 354

RESULT 7

ID CKR5_CERTO STANDARD; PRT; 352 AA.

AC 062743; 062744; 062745; 062746;

DT 15-DEC-1998 (Rel. 37, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DR C-C chemokine receptor type 5 (C-CR-5) (CC-CR-5) (CCR-5) (CCR5).

GN CCRC5 OR CMKBR5.
 OS Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Cercopithecus.
 OX NCBI_TaxID=9531;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Isolate 079, 085, 087, and 089;
 RX MEDLINE=98321155; PubMed=9656999;
 RA Chen Z., Gettie A., Ho D.D., Marx P.A.;
 RT "Primary HIVsm isolates use the CCR5 coreceptor from sooty mangabey
 RT naturally infected in west Africa: a comparison of coreceptor usage
 RT of primary HIVsm, HIV-2, and SIVmac.";
 RL Virology 246:113-124(1998).
 CC -1- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
 CC MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
 CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
 CC IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
 CC DIFFERENTIATION.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC -----
 DR EMBL; AF051902; AAC39830.1; -
 DR EMBL; AF051903; AAC39831.1; -
 DR EMBL; AF051904; AAC39832.1; -
 DR EMBL; AF051905; AAC39833.1; -
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm.1; 1.
 DR PRINTS; PR00237; GPCRHHODOPSN.
 DR PROSITE; PS00237; G-PROTEIN RECF_F1_1; 1.
 DR PROSITE; PS00237; G-PROTEIN RECF_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
 FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 31 58 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 69 89 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 103 124 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 142 166 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 199 218 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 236 260 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 278 301 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 302 352 BY SIMILARITY.
 FT DISULFID 101 178 SULFATION (BY SIMILARITY).
 FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
 FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
 FT MOD_RES 14 14 SULFATION (BY SIMILARITY).
 FT MOD_RES 15 15 SULFATION (BY SIMILARITY).
 FT VARIANT 2 2 D -> E (IN ISOLATE 087).
 FT VARIANT 3 3 Y -> D (IN ISOLATE 079).
 FT VARIANT 25 25 V -> G (IN ISOLATE 087).
 FT VARIANT 100 100 M -> K (IN ISOLATE 079).
 FT VARIANT 107 107 L -> V (IN ISOLATE 089).
 FT VARIANT 134 134 V -> G (IN ISOLATE 089).
 FT VARIANT 146 146 V -> L (IN ISOLATE 085 AND 089).
 FT VARIANT 340 340 T -> I (IN ISOLATE 079).
 SQ SEQUENCE 352 AA; 40489 MW; 20A196E2D47E49CA CRC64;

Query Match

Best Local Similarity

72.4%; Score 1376; DB 1; Length 352;

76.4%; Pred. No. 3.3e-74;

SEQUENCE FROM N.A.
SPECIES=M.mullatta; STRAIN=Indian macaque;
MEDLINE=97213934; PubMed=9060623;
Chen Z., Zhou P., Ho D.D., Landau N.R., Marx P.A.;
"Genetically divergent strains of simian immunodeficiency virus use
CCR5 as a coreceptor for entry";
J. Virol. 71:2705-2714(1997).
[3]
SEQUENCE FROM N.A.
SPECIES=M.mullatta;
MEDLINE=21354176; PubMed=11461684;
Margulies B.J., Hauer D.A., Clements J.E.;
"Identification and comparison of eleven rhesus macaque chemokine
receptors";
AIDS Res. Hum. Retroviruses 17:981-986(2001).
[4]
SEQUENCE FROM N.A.
SPECIES=M.mullatta, M.fascicularis, and M.nemestrina;
MEDLINE=97268687; PubMed=9108095;
Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
Sharron M., Samson M., Lu Z.H., Clements J.E., Murphy-Corb M.,
Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;
"Differential utilization of CCR5 by macrophage and T cell tropic
simian immunodeficiency virus strains";
Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
CC -1- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
DIFFERENTIATION
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

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DR EMBL; U77672; AAC511109.1; -
DR EMBL; U73739; AAC511158.1; -
DR EMBL; U96762; AAC34132.1; -
DR EMBL; AF005660; AAB62554.1; -
DR EMBL; AF005661; AAB62555.1; -
DR EMBL; AF005662; AAB62556.1; -
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm.1; 1.
DR PRINTS: PR00237; GPCRHHODPSN
DR PROSITE: PS00237; G-PROTEIN_RECEPTOR_F1_1; 1.
DR PROSITE: PS0262; G-PROTEIN_RECEPTOR_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT DOMAIN 1 30
FT EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 31 58
FT DOMAIN 59 68
FT CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89
FT DOMAIN 90 102
FT EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124
FT DOMAIN 125 141
FT CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 166
FT DOMAIN 167 198
FT EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 218
FT DOMAIN 219 235
FT CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 236 260
FT DOMAIN 261 277
FT EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 278 301
FT CYTOPLASMIC (POTENTIAL).
FT DOMAIN 302 352
FT BY SIMILARITY.
FT DISULFID 101 178
FT MOD_RES 3 3
FT Sulfation (BY SIMILARITY).
FT MOD_RES 10 10
FT Sulfation (BY SIMILARITY).
FT MOD_RES 14 14
FT Sulfation (BY SIMILARITY).
FT MOD_RES 15 15

FT CARBOHYD 268 268 N-LINKED (GLCNAC...) (POTENTIAL).
FT CONFLICT 241 241 M -> I (IN REF. 3).
FT CONFLICT 292 292 I -> M (IN REF. 3).
SQ SEQUENCE 352 AA; 40507 MW; 58B96C85909FACB2 CRC64;
Query Match 72.18; Score 1370; DB 1; Length 352;
Best Local Similarity 76.18; Pred. No. 7.4e-74;
Matches 261; Conservative 31; Mismatches 45; Indels 6; Gaps 2;
QY 24 FDYD--GAPCHKFDVKQIGLPPYSLVIFGVGNMVLVLLINCKLKCLTDIYL 81
Db 10 YDIYYTSEPCQKINVKQIARLLPPLSLVIFGVGNLVLVLLINCKLKSWTDIYL 69
QY 82 LNLASDLLFLITLPLWAHSAANWFGNAMCKLTGLYHIGYFGIFPIILLTIDRYLA 141
Db 70 LNLASDLLFLITLPLWAHSAANWFGNAMCKLTGLYHIGYFGIFPIILLTIDRYLA 129
QY 142 IVHAFVFAKARTVTFGVVTSVITWLVAVFASVPGVIFFTCKEDSVYVCGPYEP---RG 197
Db 130 IVHAFVFAKARTVTFGVVTSVITWLVAVFASVPGVIFFTCKEDSVYVCGPYEP---RG 189
QY 198 WNNFHTIMRNILGLVPLLLIMVICYSGILKTLRCRNEKKRHRVAVRVIPTIMIVFLFWT 257
Db 190 WKNQTLKMWILGLVPLLLIMVICYSGILKTLRCRNEKKRHRVAVRVIPTIMIVFLFWA 249
QY 258 PYNIVILLNTQEFEGLSNCESTSDQATQVTEGLMTHCCINPIIYAFVGEKPRYLS 317
Db 250 PYNIVILLNTQEFEGLSNCESTSDQATQVTEGLMTHCCINPIIYAFVGEKPRYLS 309
QY 318 VFFRKHTKRECKCPVRETVDGVTSTNTPTSGEVSAGL 360
Db 310 VFFOKHIAKRECKCSIFQQAERASSVYTRSTGEISVGL 352
RESULT 10
ID_CKR5_PANTR STANDARD; PRT; 352 AA.
AC P56440; O02778;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
GN CCR5 OR CMK9R5.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97268687; PubMed=9108095;
RA Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
RA Sharron M., Samson M., Lu Z.H., Clements J.E., Murphy-Corb M.,
RA Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;
RA "Differential utilization of CCR5 by macrophage and T cell tropic
simian immunodeficiency virus strains";
Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX Zimmermann P.A., Buckler-white A., Alkhatib G.;
RA Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=98022612; PubMed=9359654;
RA Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,
RA Ho D.D.;
RA "HIV type 1 subtypes, coreceptor usage, and CCR5 polymorphism";
AIDS Res. Hum. Retroviruses 13:1357-1366(1997).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=97426118; PubMed=9282822;
RA Zacharova V., Zachar V., Goustin A.S.;
RA "Sequence of chemokine receptor gene CCR5 in chimpanzees, a natural
HIV type 1 host.";


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FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
FT MOD_RES 14 14 SULFATION (BY SIMILARITY).
FT MOD_RES 15 15 SULFATION (BY SIMILARITY).
SQ SEQUENCE 352 AA; 40527 MW; F4E2F47135AF658A CRC64;

Query Match
Best Local Similarity 72.1%; Score 1370; DB 1; Length 352;
Matches 261; Conservative 30; Mismatches 46; Indels 6; Gaps 2;

QY 24 FDYDY--GAPCHKFDVKQIGAGLPPYSLVFIQFVGNMVLVLLINCKKLCLTDIYL 81
DQ 10 YDIYTFSEFCQKINQKQIARLLPPLYSLVFIQFVGNMVLVLLINCKKLKSMTDIYL 69
QY 82 LNLAISSLFLITLPLWAHSAANEWFGNAMCKLFTGLYHIGYFGGIFFIILLITIDRYLA 141
DQ 70 LNLAISSLFLITLPLWAHSAANEWFGNAMCKLFTGLYHIGYFGGIFFIILLITIDRYLA 129
QY 142 IVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIITFKQKEDSVVCGPYFP---RG 197
DQ 130 IVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIITFKQKEDSVVCGPYFP---RG 189
QY 198 WNNFHTIMRNILGLVPLLVIMVICYSGILKTLRCRNEKRRHRAVRVFTIMIVYELFWT 257
DQ 190 WNNFHTIMRNILGLVPLLVIMVICYSGILKTLRCRNEKRRHRAVRVFTIMIVYELFWT 249
QY 258 PYNIVILLNTFQFGLSNCESTSQLDQATQVTTGLMTHCCINPIIYAFVGEKFRYLS 317
DQ 250 PYNIVILLNTFQFGLSNCESTSQLDQATQVTTGLMTHCCINPIIYAFVGEKFRYLS 309
QY 318 VFERKHITKRCCKQCPVEYRETVGVTSTNTPTSTGEQEVSNAGL 360
DQ 310 VFERKHITKRCCKQCPVEYRETVGVTSTNTPTSTGEQEVSNAGL 352

RESULT 12
ID CKR5_GORGO STANDARD; PRT; 352 AA.
AC P56439.
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE C-C chemokine receptor type 5 (C-CR-5) (CCR-5) (CCR5).
GN CKR5 OR CMKR5.
OS Gorilla gorilla gorilla (Lowland gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
OX NCBI_TaxID=9595;
SQ SEQUENCE FROM N.A.
MEDLINE=97268687; PubMed=9108095;
RA Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
RA Sharron M., Samson M., Lu Z.H., Clements J.E., Murphy-Corb M.,
RA Pelper S.C., Parmentier M., Broder C.C., Doms R.W.;
RT "Differential utilization of CKR5 by macrophage and T cell tropic
RT simian immunodeficiency virus strains."
RL Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
CC -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
CC MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
CC IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
CC DIFFERENTIATION.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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DR EMBL; AF005659; AAB62553 1; -
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsin.
DR PROSITE; PS00237; G-PROTEIN_RECEP_FL1; 1.
DR PROSITE; PS00262; G-PROTEIN_RECEP_FL2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 31 58 1 (POTENTIAL).
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 166 4 (POTENTIAL).
FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 218 5 (POTENTIAL).
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 236 260 6 (POTENTIAL).
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 278 301 7 (POTENTIAL).
FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
FT MOD_RES 14 14 SULFATION (BY SIMILARITY).
FT MOD_RES 15 15 SULFATION (BY SIMILARITY).
SQ SEQUENCE 352 AA; 40515 MW; D0B6FCB9F5EAC84 CRC64; 1

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Query Match 72.0%; Score 1368; DB 1; Length 352;
Best Local Similarity 76.1%; Pred. No. 9.6e-74;
Matches 261; Conservative 30; Mismatches 46; Indels 6; Gaps 2;

QY 24 FDYDY--GAPCHKFDVKQIGAGLPPYSLVFIQFVGNMVLVLLINCKKLCLTDIYL 81
DQ 10 YDIYTFSEFCQKINQKQIARLLPPLYSLVFIQFVGNMVLVLLINCKKLKSMTDIYL 69
QY 82 LNLAISSLFLITLPLWAHSAANEWFGNAMCKLFTGLYHIGYFGGIFFIILLITIDRYLA 141
DQ 70 LNLAISSLFLITLPLWAHSAANEWFGNAMCKLFTGLYHIGYFGGIFFIILLITIDRYLA 129
QY 142 IVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIITFKQKEDSVVCGPYFP---RG 197
DQ 130 IVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIITFKQKEDSVVCGPYFP---RG 189
QY 198 WNNFHTIMRNILGLVPLLVIMVICYSGILKTLRCRNEKRRHRAVRVFTIMIVYELFWT 257
DQ 190 WNNFHTIMRNILGLVPLLVIMVICYSGILKTLRCRNEKRRHRAVRVFTIMIVYELFWT 249
QY 258 PYNIVILLNTFQFGLSNCESTSQLDQATQVTTGLMTHCCINPIIYAFVGEKFRYLS 317
DQ 250 PYNIVILLNTFQFGLSNCESTSQLDQATQVTTGLMTHCCINPIIYAFVGEKFRYLS 309
QY 318 VFERKHITKRCCKQCPVEYRETVGVTSTNTPTSTGEQEVSNAGL 360
DQ 310 VFERKHITKRCCKQCPVEYRETVGVTSTNTPTSTGEQEVSNAGL 352

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RESULT 13
ID CKR5_PAPHA STANDARD; PRT; 352 AA.
AC P56441;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE C-C chemokine receptor type 5 (C-CR-5) (CCR-5) (CCR5).
GN CKR5 OR CMKR5
OS Papio hamadryas (Hamadryas baboon), and
OS Papio anubis (Olive baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Papio.
OX NCBI_TaxID=9557, 9555;

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RA Muzny D., Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M.,
RA Porcel B.M., Dragan Y., Giacalone J., Pae A., Powell E.,
RA Solinsky K.A., Desilva U., Diaz-Perez S., Zhou X., Yu Y.,
RA Watanabe M., Doggett N., Garcia D., Sagripanti J.L.,
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE-98001387; PubMed-9343222;
RA Kuhlmann S.E., Platt E.J., Kozak S.L., Kabat D.,
RT "polymorphisms in the CCR5 genes of African green monkeys and mice
RT implicate specific amino acids in infections by simian and human
RT immunodeficiency viruses.";
RL J. Virol. 71:8642-8656(1997).
RN [6]
RP SEQUENCE FROM N.A., AND POLYMORPHISMS.
RX MEDLINE-98022612; PubMed-9359654;
RA Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,
RA Ho D.D.,
RT "HIV type 1 subtypes, coreceptor usage, and CCR5 polymorphism.";
RT AIDS Res. Hum. Retroviruses 13:1357-1366(1997).
RN [7]
RP SEQUENCE FROM N.A.
RX MEDLINE-98049523; PubMed-9388201;
RA Mummidi S., Ahuja S.S., McDaniel B.L., Ahuja S.K.,
RT "The human CC chemokine receptor 5 (CCR5) gene. Multiple transcripts
RT with 5'-end heterogeneity, dual promoter usage, and evidence for
RT polymorphisms within the regulatory regions and non-coding exons.";
RL J. Biol. Chem. 272:30662-30671(1997).
RN [8]
RP SEQUENCE FROM N.A., AND VARIANT ARG-178.
RA Magierowska M., Barre-Sinoussi F., Issafras H., Theodorou I.,
RA Debre P.,
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
RN [9]
RP CHARACTERIZATION OF ITS HIV-1 RECEPTOR FUNCTION.
RX MEDLINE-96260017; PubMed-8649511;
RA Deng H., Liu R., Ellmeier W., Choe S., Unutmaz D., Burkhart M.,
RA de Marzio P., Martin S.R., Hill C.M., Davis C.B.,
RA Peiper S.C., Schall T.J., Littman D.R., Landau N.R.,
RT "Identification of a major co-receptor for primary isolates of
RT HIV-1.";
RL Nature 381:661-666(1996).
RN [10]
RP CHARACTERIZATION OF ITS HIV-1 RECEPTOR FUNCTION.
RX MEDLINE-96260018; PubMed-8649512;
RA Dragic T., Littwin V., Allaway G.P., Martin S.R., Huang Y.,
RA Nagashima K.A., Cayanan C., Maddon P.J., Koup R.A., Moore J.P.,
RA Paxton W.A.,
RT "HIV-1 entry into CD4+ cells is mediated by the chemokine receptor
RT CC-CKR-5.";
RL Nature 381:667-673(1996).
RN [11]
RP SULFATION.
RX MEDLINE-99189752; PubMed-10089882;
RA Farzan M., Mirzabekov T., Kolchinsky P., Wyatt R., Cayabyab M.,
RA Gerard N.P., Gerard C., Sodroski J., Choe H.,
RT "Tyrosine sulfation of the amino terminus of CCR5 facilitates HIV-1
RT entry.";
RL Cell 96:667-676(1999).
RN [12]
RP FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
CC MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
CC IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
CC DIFFERENTIATION. ACTS AS CO-RECEPTOR WITH CD4 FOR PRIMARY NON-
CC SYNCYTUM-INDUCING STRAINS (NSI) (MACROPHAGE-TROPIC) OF HIV-1
CC VIRUS. IT PROMOTES ENV-MEDIATED FUSION OF THE VIRUS.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: FOUND IN PROMYELOCYTIC CELLS.
CC -!- PTM: SULFATION CONTRIBUTES TO THE EFFICIENCY OF HIV-1 ENTRY.
CC -!- PTM: MODIFIED BY O-LINKED GLYCOSYLATION, BUT NOT BY N-LINKED
CC GLYCOSYLATION.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

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CC DR EMBL; X91492; CAA62796.1; -
CC DR EMBL; U54994; AAC50598.1; -
CC DR EMBL; U57840; AAB17071.1; -
CC DR EMBL; U95626; AAB57793.1; -
CC DR EMBL; U83326; AAG51797.1; -
CC DR EMBL; AF011500; AAB65700.1; -
CC DR EMBL; AF011501; AAB65701.1; -
CC DR EMBL; AF011502; AAB65702.1; -
CC DR EMBL; AF011503; AAB65703.1; -
CC DR EMBL; AF011505; AAB65705.1; -
CC DR EMBL; AF011506; AAB65706.1; -
CC DR EMBL; AF011507; AAB65707.1; -
CC DR EMBL; AF011508; AAB65708.1; -
CC DR EMBL; AF011509; AAB65709.1; -
CC DR EMBL; AF011510; AAB65710.1; -
CC DR EMBL; AF011511; AAB65711.1; -
CC DR EMBL; AF011512; AAB65712.1; -
CC DR EMBL; AF011513; AAB65713.1; -
CC DR EMBL; AF011514; AAB65714.1; -
CC DR EMBL; AF011515; AAB65715.1; -
CC DR EMBL; AF011516; AAB65716.1; -
CC DR EMBL; AF011517; AAB65717.1; -
CC DR EMBL; AF011518; AAB65718.1; -
CC DR EMBL; AF011519; AAB65719.1; -
CC DR EMBL; AF011520; AAB65720.1; -
CC DR EMBL; AF011521; AAB65721.1; -
CC DR EMBL; AF011522; AAB65722.1; -
CC DR EMBL; AF011523; AAB65723.1; -
CC DR EMBL; AF011524; AAB65724.1; -
CC DR EMBL; AF011525; AAB65725.1; -
CC DR EMBL; AF011526; AAB65726.1; -
CC DR EMBL; AF011527; AAB65727.1; -
CC DR EMBL; AF011528; AAB65728.1; -
CC DR EMBL; AF011529; AAB65729.1; -
CC DR EMBL; AF011530; AAB65730.1; -
CC DR EMBL; AF011531; AAB65731.1; -
CC DR EMBL; AF011532; AAB65732.1; -
CC DR EMBL; AF011533; AAB65733.1; -
CC DR EMBL; AF011534; AAB65734.1; -
CC DR EMBL; AF011535; AAB65735.1; -
CC DR EMBL; AF011536; AAB65736.1; -
CC DR EMBL; AF011537; AAB65737.1; -
CC DR EMBL; AF031237; AAB94735.1; -
CC DR EMBL; AF052539; AAD18131.1; -
CC DR EMBL; HGNC:1606; CCR5.
CC MIM; 601373; -
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm_1; 1.
CC PRINTS; PR00037; GPCRHHODPSN.
CC PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
CC PROSITE; PS0262; G-PROTEIN_RECEP_F1_2; 1.
CC KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation;
CC polymorphism.
CC FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 31 58 1 (POTENTIAL).
CC FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 69 89 2 (POTENTIAL).
CC FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 103 124 3 (POTENTIAL).
CC FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 142 166 4 (POTENTIAL).
CC FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 199 218 5 (POTENTIAL).
CC FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 236 260 6 (POTENTIAL).

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FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 278 301 7 (POTENTIAL).
FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
FT MOD_RES 3 3 SULFATION.
FT MOD_RES 10 10 SULFATION.
FT MOD_RES 14 14 SULFATION.
FT MOD_RES 15 15 SULFATION.
FT VARIANT 10 10 SULFATION.
FT VARIANT 29 29 /FTID-VAR_003481.
FT VARIANT 31 31 A -> S (IN DBSNP:1800939).
FT VARIANT 31 31 /FTID-VAR_011839.
FT VARIANT 31 31 R -> H (IN INCCR5-72A).

Query Match 71.8%; Score 1364; DB 1; Length 352;
Best Local Similarity 75.5%; Pred. No. 1.6e-73;
Matches 259; Conservative 32; Mismatches 46; Indels 6; Gaps 2;

QY 24 FDYDY--GAPCHKFDVKQIGAOILLPLYSLVIFGFGVGNMVLVLLINCKKLCGLTDIYL 81
DB 10 YDIDYTTSEPCQKVNKQIAARLLPPLYSLVIFGFGVGNMVLVLLINCKKLCGLTDIYL 69
QY 82 LNLAIISDLFLITLPLWAHSAANEWFGNAMCKLFTGLYHIGYFGGFIIFILLTIDRYLA 141
DB 70 LNLAIISDLFLITLPLWAHSAANEWFGNAMCKLFTGLYHIGYFGGFIIFILLTIDRYLA 129
QY 142 IVHAFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCKEDSVYVCGPYFP----RG 197
DB 130 VVHAFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCKEDSVYVCGPYFP----RG 197
QY 198 WNNFHTIMRNLGLVPLLLIMVICYSGLTKLLCRNKKRRHRAVRVITIMIVFLEWT 257
DB 190 WNNFHTIMRNLGLVPLLLIMVICYSGLTKLLCRNKKRRHRAVRVITIMIVFLEWT 249
QY 258 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVETLGMTHCCINPIIYAFVGEKFRYLS 317
DB 250 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVETLGMTHCCINPIIYAFVGEKFRYLS 309
QY 318 VFRKHHTKRFCKCPVYREIVDGVTSINTPSTGGEQVSAGL 360
DB 310 VFFQKHIAKRFCKCCSIFQOEAPERASSVYTRSTGGEQVSAGL 352

RESULT 15
CKR5_TRAPH STANDARD; PRT; 352 AA.
AC 097879;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 5 (C-CR-5) (CCR-5) (CCR5).
GN CCR5 OR CMKR5.
OS Trachypithecus phayrei (Phayre's leaf monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
OC Trachypithecus.
OX NCBI_TaxID=61618;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99416438; PubMed=10486970;
RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
RL Mol. Biol. Evol. 16:1145-1154(1999).
CC -I- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
CC MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
CC IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
CC DIFFERENTIATION.
CC -I- SUBCELLULAR LOCATION: Integral membrane protein.
CC -I- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF075443; AAD19855.1;
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm1.1.
DR PRINTS: PR00237; GPCRHHODPSN.
DR PROSITE: PS00237; G-PROTEIN_RECP_FL1; 1.
DR PROSITE: PS00262; G-PROTEIN_RECP_FL2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 31 58 1 (POTENTIAL).
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 166 4 (POTENTIAL).
FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 218 5 (POTENTIAL).
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 236 260 6 (POTENTIAL).
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 278 301 7 (POTENTIAL).
FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
FT MOD_RES 14 14 SULFATION (BY SIMILARITY).
FT MOD_RES 15 15 SULFATION (BY SIMILARITY).
SQ SEQUENCE 352 AA; 40509 MW; 4366F148D3A5938F CRC64;

Query Match 71.7%; Score 1363; DB 1; Length 352;
Best Local Similarity 75.8%; Pred. No. 1.9e-73;
Matches 260; Conservative 31; Mismatches 46; Indels 6; Gaps 2;

QY 24 FDYDY--GAPCHKFDVKQIGAOILLPLYSLVIFGFGVGNMVLVLLINCKKLCGLTDIYL 81
DB 10 YDIDYTTSEPCQKVNKQIAARLLPPLYSLVIFGFGVGNMVLVLLINCKKLCGLTDIYL 69
QY 82 LNLAIISDLFLITLPLWAHSAANEWFGNAMCKLFTGLYHIGYFGGFIIFILLTIDRYLA 141
DB 70 LNLAIISDLFLITLPLWAHSAANEWFGNAMCKLFTGLYHIGYFGGFIIFILLTIDRYLA 129
QY 142 IVHAFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCKEDSVYVCGPYFP----RG 197
DB 130 IVHAFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCKEDSVYVCGPYFP----RG 197
QY 198 WNNFHTIMRNLGLVPLLLIMVICYSGLTKLLCRNKKRRHRAVRVITIMIVFLEWT 257
DB 190 WNNFHTIMRNLGLVPLLLIMVICYSGLTKLLCRNKKRRHRAVRVITIMIVFLEWT 249
QY 258 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVETLGMTHCCINPIIYAFVGEKFRYLS 317
DB 250 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVETLGMTHCCINPIIYAFVGEKFRYLS 309
QY 318 VFRKHHTKRFCKCPVYREIVDGVTSINTPSTGGEQVSAGL 360
DB 310 VFFQKHIAKRFCKCCSIFQOEAPERASSVYTRSTGGEQVSAGL 352

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